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HOW DOES SCYLV GENETIC DIVERSITY IMPACT ON SUGARCANE DISEASE RESISTANCE AND BREEDING?

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To date, six distinct genotypes of the *Sugarcane yellow leaf virus* have been described in the literature (BRA, CUB, CHN1, IND, PER and REU). However, little information is available regarding the impact of virus genetic diversity on disease resistance. Three SCYLV genetic groups that can be identified with specific primers by RT-PCR are present in Guadeloupe: BRA-PER, CUB and REU. The impact of the virus genotype diversity on rating for resistance to yellow leaf was studied on a sub-population of 40 sugarcane clones issued from a population of 200 clones planted in a complete three blocks design. The sub-population was screened for virus incidence by sampling 10 leaves per plot and detecting SCYLV by tissue blot immunoassay (TBIA). For each plot, SCYLV genotypes were diagnosed by RT-PCR in a bulk of the TBIA positive leaves. The experiment was repeated in a second crop cycle. The results gave an estimation of genotype incidences for each clone. Of the 185 samples used for SCYLV genotyping, BRA-PER was found in 105, CUB in 170 and REU in 99 samples. CUB was the most frequent genotype encountered and had the largest cultivar host range, overlapping cultivar host ranges of BRA-PER and REU. Additionally, CUB incidence gave the best correlation with SCYLV incidence in each cultivar (R^2 0.87). In addition, the incidences of virus genotypes in each cultivar compared by regression analysis showed that the incidence of CUB was correlated to the incidence of REU (R^2 0.46), whereas the correlations between the incidence of BRA-PER and the two other genotype incidences were low (R^2 of 0.12 and 0.14). In view of these results, it is suspected that plant resistance mechanisms for yellow leaf disease depend on the genotype involved and that, in Guadeloupe, we are mainly looking for resistance to CUB genotype as its incidence overlaps with the two other ones, masking resistance to REU and BRA-PER.